

## SEQUENCE LISTING

<110> The Horticulture and Food Research Institute of Ne

<120> Serine Protease Inhibitor

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<150> NZ 336906

<151> 1999-07-23

<160> 8

<170> PatentIn Ver. 2.1

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<213> Perna canaliculus

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Gly Arg Ala

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Gly Gln Ser His Pro Glu Ile Val His

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5

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&lt;213&gt; Perna canaliculus

&lt;400&gt; 4

Tyr His Gly His Asp Asp Ala

1

5

&lt;210&gt; 5

&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Perna canaliculus

&lt;400&gt; 5

Val Val Asn Glu Val His His

1

5

&lt;210&gt; 6

&lt;211&gt; 1491

&lt;212&gt; DNA

&lt;213&gt; Perna canaliculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1491)

&lt;400&gt; 6

gay ggg gag cag tgt aac gat ggg cag aac aaa gat gac cac cat gac 48

Asp Gly Glu Gln Cys Asn Asp Gly Gln Asn Lys Asp Asp His His Asp

1

5

10

15

gac cac cac gat gat cac cat gac gac cat gat gat gat gat gaa aca 96

Asp His His Asp Asp His His Asp Asp His Asp Asp Asp Asp Glu Thr

20

25

30

atg cac tat gcc cag tgt gaa atg gaa cca aac cct cat atg gct agc 144

Met His Tyr Ala Gln Cys Glu Met Glu Pro Asn Pro His Met Ala Ser

35	40	45	
agc ctt cac cac cat gtc cat ggc agc ata gag ttg tca cag aag ggt			192
Ser Leu His His His Val His Gly Ser Ile Glu Leu Ser Gln Lys Gly			
50	55	60	
cat gga gct gtt tat cta gaa ctt cat ctt gtc gga ttc aac aca agt			240
His Gly Ala Val Tyr Leu Glu Leu His Leu Val Gly Phe Asn Thr Ser			
65	70	75	80
gaa gac cat gac gac cac cat cat gga ctt cat ctg cac atg ctt ggt			288
Glu Asp His Asp Asp His His His Gly Leu His Leu His Met Leu Gly			
85	90	95	
gac atg tca gca ggt tgt gat tct att ggc gaa ctg tac aat gct cac			336
Asp Met Ser Ala Gly Cys Asp Ser Ile Gly Glu Leu Tyr Asn Ala His			
100	105	110	
cca gaa aaa cat gct gac cct ggt gac ctc ggt gac ctg gtt gac gat			384
Pro Glu Lys His Ala Asp Pro Gly Asp Leu Gly Asp Leu Val Asp Asp			
115	120	125	
gat agg ggc gtg gtt aat gaa gtt cat cat tat gct tgg ttg gac att			432
Asp Arg Gly Val Val Asn Glu Val His His Tyr Ala Trp Leu Asp Ile			
130	135	140	
gat ggt aca gca cca aac acc gaa gct ctc att gga cac tca atg act			480
Asp Gly Thr Ala Pro Asn Thr Glu Ala Leu Ile Gly His Ser Met Thr			
145	150	155	160
att tta caa ggg agt cac acc gat gct gat acc cca gcc agt aga atc			528
Ile Leu Gln Gly Ser His Thr Asp Ala Asp Thr Pro Ala Ser Arg Ile			
165	170	175	
gcc tgt tgt gtt att ggt cat gga aaa gct cgc cca gaa aca gca gct			576
Ala Cys Cys Val Ile Gly His Gly Lys Ala Arg Pro Glu Thr Ala Ala			
180	185	190	
gct cta cat cac gag cta gag gaa gat aaa act gag cat tat gcc cat			624
Ala Leu His His Glu Leu Glu Glu Asp Lys Thr Glu His Tyr Ala His			
195	200	205	
tgt gac gta aga tct aat aca cac caa cca aag gct ctt cat cat cat			672
Cys Asp Val Arg Ser Asn Thr His Gln Pro Lys Ala Leu His His His			
210	215	220	
gtc cac gga acc atc gat ttc aaa caa gtt ggt tat ggt gac ctt gaa			720
Val His Gly Thr Ile Asp Phe Lys Gln Val Gly Tyr Gly Asp Leu Glu			

225	230	235	240	
gtg tcc tac cat tta gag gga ttt aat gta agt gat gac cac aaa gat				768
Val Ser Tyr His Leu Glu Gly Phe Asn Val Ser Asp Asp His Lys Asp				
245	250	255		
cat ctc cat gac gta cag atc tac gcc aac ggt gac ctg acc agt gga				816
His Leu His Asp Val Gln Ile Tyr Ala Asn Gly Asp Leu Thr Ser Gly				
260	265	270		
tgt gat aac ctc ggt gct aaa tat gat cct cat gaa gat tac cac agt				864
Cys Asp Asn Leu Gly Ala Lys Tyr Asp Pro His Glu Asp Tyr His Ser				
275	280	285		
gag ttg ggt gat cta gga gat att cac gat gat gac cat ggc gtt gtc				912
Glu Leu Gly Asp Leu Gly Asp Ile His Asp Asp Asp His Gly Val Val				
290	295	300		
aat gaa agc cac aga tat tcc tgg atc aat atc ttc ggt gat gac agt				960
Asn Glu Ser His Arg Tyr Ser Trp Ile Asn Ile Phe Gly Asp Asp Ser				
305	310	315	320	
gtc ctg gga cgt tct att gcc att cac caa aga gac cat ctt cat aaa				1008
Val Leu Gly Arg Ser Ile Ala Ile His Gln Arg Asp His Leu His Lys				
325	330	335		
agt gcc aaa att gcc tgt tgt gtc ata gga cgt gga cag agc cat cca				1056
Ser Ala Lys Ile Ala Cys Cys Val Ile Gly Arg Gly Gln Ser His Pro				
340	345	350		
gaa att gtt cac aga gct aaa tgt gtt gtc aga cct aat aca gaa tct				1104
Glu Ile Val His Arg Ala Lys Cys Val Val Arg Pro Asn Thr Glu Ser				
355	360	365		
act ggt tta cat cac cat gtc tct ggt tct ata aca ttc gaa cag acc				1152
Thr Gly Leu His His His Val Ser Gly Ser Ile Thr Phe Glu Gln Thr				
370	375	380		
cct gga gga tca aca cat atg acg gct gat ctc aaa gga ttt aac gtt				1200
Pro Gly Gly Ser Thr His Met Thr Ala Asp Leu Lys Gly Phe Asn Val				
385	390	395	400	
agt gag gac ttg tca cat cat cgt cat ggt gtg cag ctc cat gaa tgg				1248
Ser Glu Asp Leu Ser His His Arg His Gly Val Gln Leu His Glu Trp				
405	410	415		
gga gat atg tcc cat ggc tgt cac tcc tta ggc aga atg tac cat ggt				1296
Gly Asp Met Ser His Gly Cys His Ser Leu Gly Arg Met Tyr His Gly				



420	425	430	
cat gat gat gct cat gac ccc aaa aga cct ggt gac ctt ggt gat gtt			1344
His Asp Asp Ala His Asp Pro Lys Arg Pro Gly Asp Leu Gly Asp Val			
435	440	445	
ata gat gat tcc cat ggc atc gtt cat tca act aga acc ttt gat cat			1392
Ile Asp Asp Ser His Gly Ile Val His Ser Thr Arg Thr Phe Asp His			
450	455	460	
ctt aat gtt gaa gat ctt aac gca cgt tcc ctt gtg att atg cag ggc			1440
Leu Asn Val Glu Asp Leu Asn Ala Arg Ser Leu Val Ile Met Gln Gly			
465	470	475	480
gga cat gag gtc gag agt gag agg gtt gct tgc tgt gtt ata gga cgg			1488
Gly His Glu Val Glu Ser Glu Arg Val Ala Cys Cys Val Ile Gly Arg			
485	490	495	
gca			1491
Ala			
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Asp His His Asp Asp His His Asp Asp His Asp Asp Asp Asp Glu Thr			
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Met His Tyr Ala Gln Cys Glu Met Glu Pro Asn Pro His Met Ala Ser			
35	40	45	
Ser Leu His His His Val His Gly Ser Ile Glu Leu Ser Gln Lys Gly			
50	55	60	
His Gly Ala Val Tyr Leu Glu Leu His Leu Val Gly Phe Asn Thr Ser			
65	70	75	80
Glu Asp His Asp Asp His His His Gly Leu His Leu His Met Leu Gly			
85	90	95	
Asp Met Ser Ala Gly Cys Asp Ser Ile Gly Glu Leu Tyr Asn Ala His			
100	105	110	

Pro Glu Lys His Ala Asp Pro Gly Asp Leu Gly Asp Leu Val Asp Asp  
115 120 125

Asp Arg Gly Val Val Asn Glu Val His His Tyr Ala Trp Leu Asp Ile  
130 135 140

Asp Gly Thr Ala Pro Asn Thr Glu Ala Leu Ile Gly His Ser Met Thr  
145 150 155 160

Ile Leu Gln Gly Ser His Thr Asp Ala Asp Thr Pro Ala Ser Arg Ile  
165 170 175

Ala Cys Cys Val Ile Gly His Gly Lys Ala Arg Pro Glu Thr Ala Ala  
180 185 190

Ala Leu His His Glu Leu Glu Glu Asp Lys Thr Glu His Tyr Ala His  
195 200 205

Cys Asp Val Arg Ser Asn Thr His Gln Pro Lys Ala Leu His His His  
210 215 220

Val His Gly Thr Ile Asp Phe Lys Gln Val Gly Tyr Gly Asp Leu Glu  
225 230 235 240

Val Ser Tyr His Leu Glu Gly Phe Asn Val Ser Asp Asp His Lys Asp  
245 250 255

His Leu His Asp Val Gln Ile Tyr Ala Asn Gly Asp Leu Thr Ser Gly  
260 265 270

Cys Asp Asn Leu Gly Ala Lys Tyr Asp Pro His Glu Asp Tyr His Ser  
275 280 285

Glu Leu Gly Asp Leu Gly Asp Ile His Asp Asp Asp His Gly Val Val  
290 295 300

Asn Glu Ser His Arg Tyr Ser Trp Ile Asn Ile Phe Gly Asp Asp Ser  
305 310 315 320

Val Leu Gly Arg Ser Ile Ala Ile His Gln Arg Asp His Leu His Lys  
325 330 335

Ser Ala Lys Ile Ala Cys Cys Val Ile Gly Arg Gly Gln Ser His Pro  
340 345 350

Glu Ile Val His Arg Ala Lys Cys Val Val Arg Pro Asn Thr Glu Ser  
355 360 365

Thr Gly Leu His His His Val Ser Gly Ser Ile Thr Phe Glu Gln Thr  
 370 375 380

Pro Gly Gly Ser Thr His Met Thr Ala Asp Leu Lys Gly Phe Asn Val  
 385 390 395 400

Ser Glu Asp Leu Ser His His Arg His Gly Val Gln Leu His Glu Trp  
 405 410 415

Gly Asp Met Ser His Gly Cys His Ser Leu Gly Arg Met Tyr His Gly  
 420 425 430

His Asp Asp Ala His Asp Pro Lys Arg Pro Gly Asp Leu Gly Asp Val  
 435 440 445

Ile Asp Asp Ser His Gly Ile Val His Ser Thr Arg Thr Phe Asp His  
 450 455 460

Leu Asn Val Glu Asp Leu Asn Ala Arg Ser Leu Val Ile Met Gln Gly  
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Gly His Glu Val Glu Ser Glu Arg Val Ala Cys Cys Val Ile Gly Arg  
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<210> 8

<211> 1611

<212> DNA

<213> Perna canaliculus

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<222> (1557)..(1563)

<220>

<221> misc\_feature

<222> (1492)..(1494)

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 gaaccaaacc ctcatatggc tagcagcctt caccaccatg tccatggcag catagagttg 180

tcacagaagg gtcattggagc tgtttatcta gaacttcac tttgtcggatt caacacaagt 240  
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tggttggaca ttgatgggtac agcaccaaac accgaagctc tcattggaca ctcaatgact 480  
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aaacaatgac acaatgnaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1611